

ERRATUM

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Erratum to: 'Reference-free inference of tumor phylogenies from single-cell sequencing data'

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Unfortunately, the original version of this article [1] contained an error. Figures 2, 4 and 5 were incorrect and the captions for Figs. 4 and 5 were incorrect. Below are the correct figures and captions:

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Reference

1. Schwartz R, Subramanian A. Reference-free inference of tumor phylogenies from single-cell sequencing data'. *BMC Genomics*. 2015;16 Suppl 11:S7.

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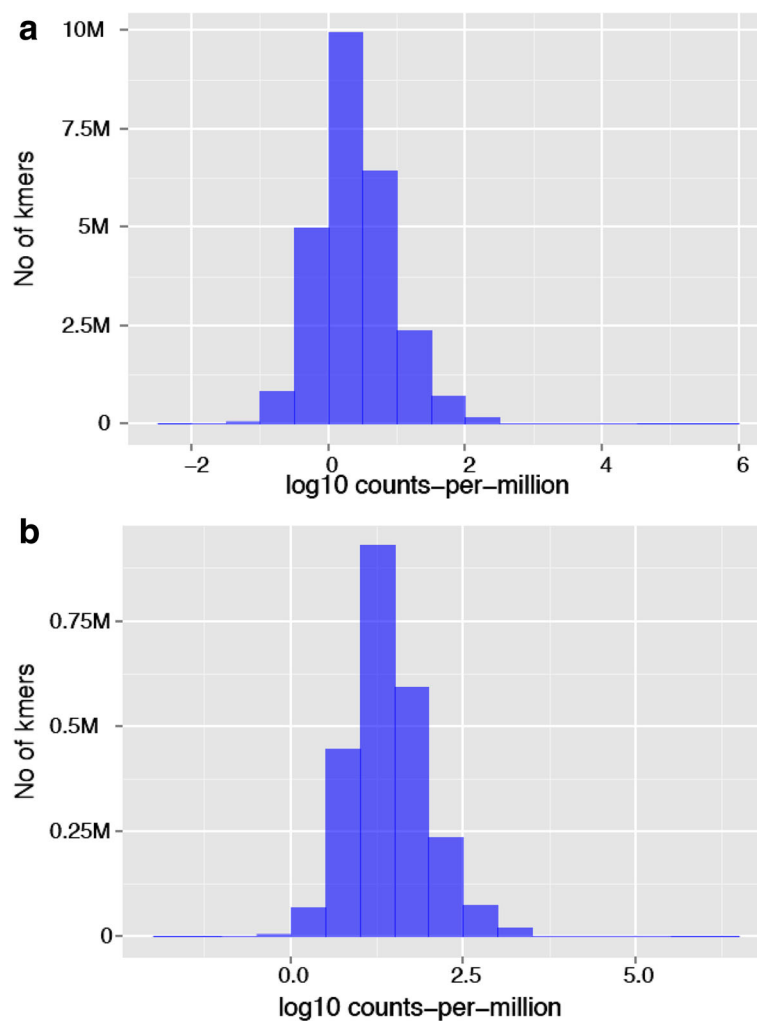


Fig. 2 Histogram of k-mer relative abundances. Both 20- and 25-mer relative abundance densities appear log-laplacian. These data included 20- and 25-mers found in all tumor cells. **a** Histogram of 20-mer relative abundances in log10 scale. **b** Histogram of 25-mer relative abundances in log10 scale

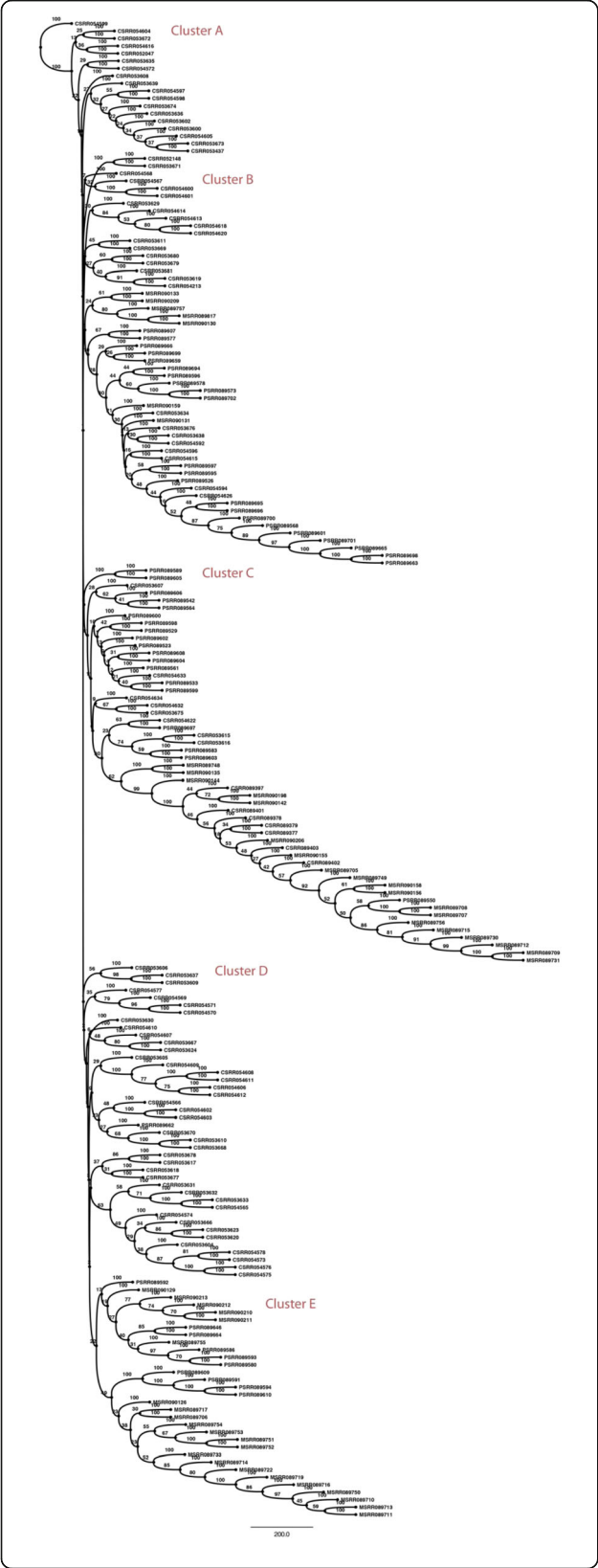


Fig. 4 20-mer bootstrap consensus neighbor-joining tree built from T10 primary breast tumor cells (prefix C), T16 primary (prefix P) and metastatic data (prefix M). Distinct groupings of cells are labeled as clusters

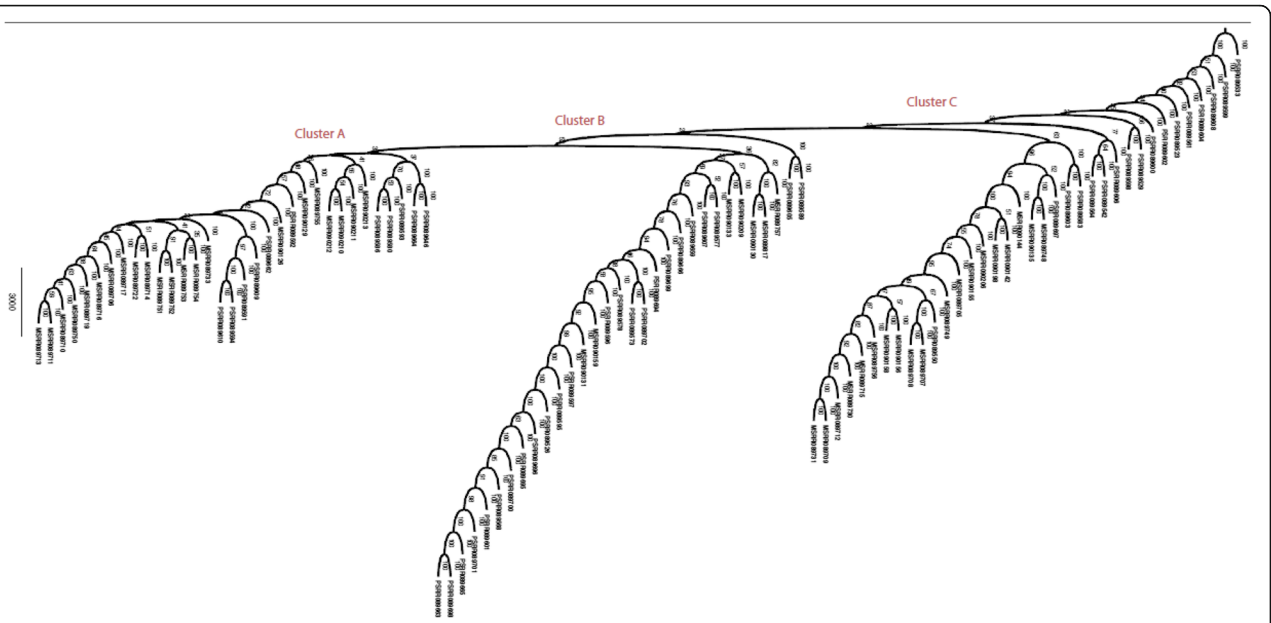


Fig. 5 20-mer bootstrap consensus neighbor-joining tree built from T16 primary (prefix P) and metastatic data (prefix M). Distinct groupings of cells are labeled as clusters